Fr m: Sent:

Bunner, Bridget

Friday, August 02, 2002 4:31 PM STIC-Biotech/ChemLib

Subject:

sequence search

10/10/2000

Hi! I'd like to request a sequence search for case 09/686,020:

1. the amino acid sequence of SEQ ID NO: 2

10/12/1999

Thanks!

Bridget Bunner

Art Unit 1647 CM1-10D12 (703) 305-7148 mailbox 10B19

> 09/721,341 Agle consider mating 103 12-1

Point of Contact: Toby Port Technical Info. Specialist CM1 6A04 703-308-3534

Searcher:
Phone:
Location:
Date Picked Up: <u>8ん</u>
Date Completed:う/つ
Searcher Prep/Review:/
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences: /
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where app	olic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (specify):	

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Appl Appli Appli Appli Appli Appli Appli

Sequence Seq Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence 4 Sequence 4 Sequence 6

Appli Appli Appli Appli Appli Appli Appli Appli

Sequence 1, Sequence 8,

Sequence Sequence 8 Sequence

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APPLICANT: La1, Preeti
APPLICANT: La1, Preeti
APPLICANT: Redy, Roopa
APPLICANT: Reddy, Roopa
APPLICANT: Mathur, Lynn E.
APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                   US-09-116-498-4
US-09-116-498-6
US-09-275-3848-5
US-09-116-498-2
US-09-116-498-2
US-09-875-573-20
US-09-232-878-2
                                                                                                                                                                                                                                                                      US-09-045-583-55
US-07-759-568-1
US-08-450-393A-8
US-08-390-000A-5
                       US-09-178-637-2
US-09-045-583-48
                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-00476-8
US-08-202-056-7
                                                                                                                                                                                                                                                                                                                                                                            US-08-446-669-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET WUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08966316
Patent No. 5932445
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIMBELATE: OUTRSNOT11
CLONE: 2547002
US-08-966-316-16
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Sequence 19,
Sequence 19,
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Sequence 19,
Sequence 15,
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-966-316-18

US-08-153-848-19

US-09-088-337B-19

US-08-153-848-15

US-09-299-843A-15

US-09-291-843A-15

US-09-291-843A-15

US-09-291-843A-15

US-09-088-337B-15

US-09-088-337B-7

US-09-088-337B-7

US-09-088-337B-7

US-09-088-337B-6

US-09-088-337B-6

US-09-088-337B-6

US-09-088-337B-6

US-09-088-337B-6

US-09-088-337B-6

US-09-088-337B-6

US-09-088-337B-2

US-09-156-464-2

US-09-266-464-2

US-09-266-464-2

US-09-266-464-2

US-09-266-464-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1819
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Match Length
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Perfect score:
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                                                          1 MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
                                                                            1 MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLIVFVIGLAGNS 60
                               Gaps
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Length 350;
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APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn E.
APPLICANT: Mathur, Preete
APPLICANT: Mathur, Preete
AITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
SIRRET: 3174 Porter Drive
                               Indels
 100.0%; Score 1819; DB 2;
100.0%; Pred. No. 7.6e-148;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
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Patent No. 5932445
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-055
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARRCTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
    Query Match
Best Local Similarity 100.
Matches 350; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Godska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell,
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                      .;
0
                                                                                                                                                  Length 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 ILYVEMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
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                                                                                                                                                                                    22;
                                                                                                                                              89.1%; Score 1620; DB 2;
86.0%; Pred. No. 7.1e-131;
iive 27; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/POCKET NUMBER: 31794
TELECHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                              Ouery Match
Best Local Similarity 86.0°
Matches 301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60606
COMPUTER READABLE FORM:
STRANDEDNESS: single
                    TCPOLOGI: Linear,
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 399711
US-08-966-316-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-153-848-19
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FILING DATE:
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US-09-088-337B-19
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                                                                                                                                                                                                                                                                                                                                                                                                                          177 TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 DLORSSSEQAMRCSLITEH---VEAFITIOVAOMVIGFLVPLLAMSFCYLVIIRTLLQAR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 ALFHSCLNPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 ACVRCCVNPFLYAFIGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVE---- 349
                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                    APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  38;
                                                                                                                                                                                               Length 358;
                                                                                                                                                                                            36.2%; Score 659; DB 1; Length 358.38.7%; Pred. No. 6.7e-49; live 66; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
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APPLICATION NUMBER: US/09/299,843A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-299-843A-19
: Sequence 19, Application US/09299843A
: Patent No. 6107475
: GENERAL INFORMATION:
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
                                                                                                                                                                                            Ouery Match
Best Local Similarity 38.7%
Matches 144; Conservative
                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein US-08-153-848-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
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61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 ACVRCCVNPFLYAFIGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVE---- 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 ALFHSCLNPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.2%; Score 659; DB 3; Length 350
38.7%; Pred. No. 6.7e-49;
.1ve 66; Mismatches 124; Indels
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STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                         NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFRENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6300
         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 358 amino acids TYPE: amino acid
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.2%; Score 659; DB 4; Length 35 38.7%; Pred. No. 6.7e-49; Live 66; Mismatches 124; Indels
                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                    PRIOR DATE: 01-Jun-1998
CLASSIFICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION OF CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1800
TELEFRAN: (312) 474-6300
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-088-3378-19
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GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 358 amino acids TYPE: amino acid
                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
ZIP: 60606
COMPUTER READABLE FORM:
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Best Local Similarity 38.79
Matches 144; Conservative
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PCT-US93-11153-19
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61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLETLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALFHSCLNPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD
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Best Local Similarity 38.7%; Pred. No. 6.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38;
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE DOCKET NUMBER: 31794
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELERAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARATERISTICS:
LENGTH: 358 amino acids
                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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amino acid
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; MOLECULE TYPE: protein
PCT-US93-11153-19
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                       CITY: Chicago
STATE: Illinois
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61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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315 ACVRCCVNPFLYAFIGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVE---- 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 VCLCQDEVTDDYIGDNT---TVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Godisk, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: NO. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 378;
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38.7%; Pred. No. 7.1e-49;
.ive 66; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago CITY: 111inois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/09299843A Patent No. 6107475 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 378 amino acids
amino acid
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                                                                         338 SEGPTEPTSTFS 349
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----AETTTTFS 377
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90909
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APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick with the septiment of the septiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804 and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/08153848 Patent No. 5759804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (312) 474-6300
TELEFRX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acid
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 15:
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                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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Best Local Similarity 38.78
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
 SEGPTEPTSTFS 349
                                ----AETTTIES 377
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                                                                                                    US-09-088-337B-15
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                                                                      MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                                                TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP
                                                                                                                    232 NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI
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APPLICANT: Edward R. Appelbaum
APPLICANT: Edward R. Appelbaum
APPLICANT: Henry M. Sarau
APPLICANT: Hory M. Sarau
APPLICANT: Hory M. Sarau
TITLE OF INVENTION: MTHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN
TITLE OF INVENTION: AND CK -9 LIGAND AND INTERACTION THEREOF
FILE REFERENCE: P50753
CURRENT FILING DATE: 1999-02-17
EARLIER APPLICATION NUMBER: 60/074,883
EARLIER APPLICATION NUMBER: 60/074,883
EARLIER FILING DATE: 1998-02-17
NUMBER OF SEO ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.2%; Score 659; DB 4; Length 378 38.7%; Pred. No. 7.1e-49; ive 66; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09251545 Patent No. 6153441
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370 ----AETTTTFS 377
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LENGTH: 378
TYPE: PRT
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61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schwelkart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 378;
                                                                                                                                                                                                                                                                                      STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.2%; Score 659; DB 4; Length 37:
38.7%; Pred. No. 7.1e-49;
Live 66; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                        Gerstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
02-09-088-3378-15
                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole,
Sequence 15, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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us-09-686-020a-2.rai

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121 LNFVSGMOFLACISIDRYVAVTKVPS----QSGVGKPCWIICFCVWMAAILLSIPQLVFY 176
                        292 ALFHSCLNPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD 337
                                                                                                                                                                                                                                                                TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP 231
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                                                                                                                                                           NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 659; DB 1; I
Pred. No. 7.8e-49;
; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTOCNEY/AGENT INFORMATION:
NAME: NO. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
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38.7%; Prec
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Patent No. 5759804
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
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TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 38.7%
Matches 144; Conservative
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370 ----AETTTTES 377
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COUNTRY: USA
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                                                            292 ALFHSCLNPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD 337
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                                     232 NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI
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                                                                                                                                                                                                                                                                                                                            Sequence 15, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godlaka, Ronald
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
TUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORNATION:
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REGISTRATION NUMBER: 35,302
REPERCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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; MOLECULE TYPE: protein
PCT-US93-11153-15
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COUNTRY: USA
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US-09-088-337B-7
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MVVALYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                                                                                                               177 TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP 231
                                                                                                                                                                          NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI 291
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                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA
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ER: 27866/32059B
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CLASSIETCATION: 435
PRIOR APPLICATION DATE:
APPLICATION DATE:
TILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1993
ATTORNEY, AGENT: 17-NOV-1993
ATTORNEY, AGENT: 17-NOV-1993
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (312) 474-0448
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
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----AETTTTFS 409
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SOFTWARE: PatentI
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61 MVVALYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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                                                                                                                                                          Length 410;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,3378
                                                                                                                                                  ; Score 659; DB 3; L
; Pred. No. 7.8e-49;
66; Mismatches 124;
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APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
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CLASSIFICATION: <Unknown>
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                                                                                                                                                  Query Match
Best Local Similarity 38.7%;
Matches 144; Conservative 66
     ; TYPE: amino acids; TYPE: amino acids; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-299-843A-7
SEQUENCE CHARACTERISTICS
LENGTH: 410 amino acid
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STATE: Illinois
COUNTRY: USA
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Search completed: August 6, 2002, 18:08:28 Job time: 238 sec
                                         APPLICATION NUMBER: PCT/US93/11153
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Best Local Similarity 38.7%
Matches 144; Conservative
                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.2%; Score 659; DB 4; Length 410; 38.7%; Pred. No. 7.8e-49; tive 66; Mismatches 124; Indels
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GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6300 Sears Tower, 233 South Wacker Drive
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
ATTORNEY/AGENT INFORMATION:

NAME: NO. 6448574and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELEPOMMUNICATION INFORMATION:

TELEPAX: (312) 474-6300

TELEPX: (312) 474-6448

TELEX: 25-3856

INFORMATION FOR SEO ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 410 mmino acids
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-088-3378-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 38.7%
Matches 144; Conservative
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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LNFVSGMQFLACISIDRYVAVTKVPS----QSGVGKPCWIICFCVWMAAILLSIPQLVFY 176
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38.7%; Pred. No. 7.8e-49;
ive 66; Mismatches 124; Indels
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
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Wed Aug

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 6, 2002, 18:07:30 ; Search time 13.42 Seconds (without alignments) 1009.824 Million cell updates/sec Run on:

US-09-686-020A-2 1819 1 MALEQNQSTDYYXEENEMNG.....VEEFPFDSEGPTEPTST 350 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9npb9 homo sapien	bos t	P32248 homo sapien	P47774 mus musculu	O9wut7 mus musculu	P51686 homo sapien	mus m	4	-	Q9xt45 macaca mula	macac	homod	homo	homod	pan t	рошо	rattu	000590 homo sapien	-	P49238 homo sapien	P51680 mus musculu	Q28519 macaca mula	Q9j121 mus musculu	097571 canis famil	Q9z0d9 mus musculu	P35344 oryctolagus	33	P21109 oryctolagus	cavi	7	soq (28003 bos ta	P56491 papio anubi
SUMMARIES	ID	CKRB_HUMAN	CKRB_BOVIN	CKR7_HUMAN	CKR7_MOUSE	CKR9_MOUSE	CKR9_HUMAN	CKR6_MOUSE	CKR6_HUMAN	CCR6_CERAE	CCR6_MACMU	CCR6_MACNE	CCR6_HUMAN	CKR4_HUMAN	IL8B_HUMAN	IL8B_PANTR	CKRA_HUMAN	C3X1_RAT	CKD6_HUMAN	IL8B_GORGO	C3X1_HUMAN	CKR4_MOUSE	IL8B_MACMU	CKRA_MOUSE	IL8B_CANFA	C3X1_MOUSE	IL8B_RABIT	CKR2_MACMU	IL8A_RABIT	CKR3_CAVPO	CCR4_HUMAN	CCR4_BOVIN	IL8B_BOVIN	CCR4_PAPAN
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062743 cercocebus	P56498 felis silve	P55919 gorilla gor	P56493 cercopithec	062747 cercocebus	Q28474 macaca fasc	P79394 macaca mula	O54814 rattus norv	P35407 rattus norv	P56441 papio hamad	097880 pygathrix b	P79436 macaca mula
CKR5_CERTO	CCR4_FELCA	IL8A_GORGO	CKR5_CERAE	CCR4_CERTO	CCR4_MACFA	CCR4_MACMU	CKR3_RAT	IL8B_RAT	CKR5_PAPHA	CKR5_PYGBI	CKR5_MACMU
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352	353	350	352	352	352	352	359	359	352	352	352
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ALIGNMENTS

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Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
BY SIMILARITY.
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ID CKRB_BOVIN

CKRB_BOVIN

P35360;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last amoutation update)

DE C-C chemokine receptor type 11 (C-C CKR-11) (CCR-11)

DE C-C chemokine receptor type B) (PPR1 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1819; DB 1; Length 350; 100.0%; Pred. No. 1.3e-104; Live 0; Mismatches 0; Indels 0
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1 42 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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InterPro; IPR000276; GPCR_Rhodpsn.
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Best Local Similarity 100.
Matches 350; Conservative
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61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
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89.1%; Score 1620; DB 1; Length 350;
Best Local Similarity 86.0%; Pred. No. 1.8e-92;
Matches 301; Conservative 27; Mismatches 22; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50263; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation.
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELUCIAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S63848; AAB27547.1; -.
BIT; JN0621; JN0621.
GCRDb; GCR_0757; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                        01-0CT-1993 (Rel. 27, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 7 precursor (C-C CKR-7) (CC-CKR-7) (CCR-7)
(MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR OF BY EFFECTS ON B LYMPHOCYTES OR OF NORWAL LYMPHOCYTE FUNCTIONS. SUBCELLULAR LOCATION: INLEGAIL MEMBRANE PICOLELI.

TISSUE SPECIFICITY: EXPRESSED IN WARLOUS LYMPHOLD TISSUES AND ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Placenta;
MEDLINE-95154835; PubMed-7851893;
Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
Schwes T.B., Gray P.W.;
"Cloning of human and mouse EBII, a lymphoid-specific
G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
Genomics 23:643-650(1994).
           300
                      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
          241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNP
                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFECTED WITH EPSTEIN-BARR VIRUS AND T CELLS INFECTED WITH HERPESVIRUS 6 OR 7. INDUCTION: BY EBV.
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-93188173; Pubmed-8383238;
Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
                                                                                                                                                                                                                                                                                                                                                                        "Epstein Barr virus-induced genes: first lymphocyte-specific protein-coupled peptide receptors."; J. Virol. 67:2209-2220(1993).
                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                               378 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L08176; AAA58615.1; -.
EMBL; L31584; AAA74230.1; -.
EMBL; L31582; AAA74230.1; JOINED.
EMBL; L31583; AAA74230.1; JOINED.
EMBL; L31581; AAA74231.1; -.
PIR; A45680; A45680.
HSSP; P34996; LDDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                              CCR7 OR CMKBR7 OR EBI1 OR EVII Homo sapiens (Human).
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PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                              CKR7_HUMAN P32248;
                                                                                                                                                                                                                                                                                                                                                               Kieff E.;
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01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 7 precursor (C-C CKR-7) (CCR-7) (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LNFVSGMQFLACISIDRYVAVTKVPS----QSGVGKPCWIICFCVWMAAILLSIPQLVFY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALFHSCLNPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLONAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 378;
                                                                         C-C CHEMOKINE RECEPTOR TYPE 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66; Mismatches 124; Indels
                                                                                                         1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                         4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 D4CB4213841A1BD4 CRC64;
                                                                                                                                                                                  3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                          5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                          IW -> SA (IN REF. 1).
L -> I (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.2%; Score 659; DB 1; 38.7%; Pred. No. 7.4e-34;
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                                                          POTENTIAL.
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CCR7 OR CMKBR7 OR EBI1 OR EBI1H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   42874 MW;
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331
378
36
210
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                                                                                                                                                                                                                                                                                                                                                                                                            182
337
378 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                    protein coupled
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P47774;
                                                                                                                            DOMAIN
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CONFLICT
SEQUENCE
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TRANSMEM
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TRANSMEM
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                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
8
                                          SEQUENCE FROM N.A.
STRAIN-B66/CBA; TISSUE—Thymus;
MEDLINE-95154835; PubMed-7851893;
Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
"Cloning of human and mouse EBII, a lymphoid-specific
G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
G-Protein-coupled receptor Roy THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
I- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
I- SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 IYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 VNDNA----RCIPIFPRYLGTSMKAL--IQMLEICIGFVVPFLIMGVCYFITARTLMKM 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 QNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGMQFLACISIDRYVAVTKVPSQSG-----VGKPCWILCFCVWMAAILLSIPQLVFYT
                                                                                                                                                                                                                                                                                                                                                                                                   FIGHTS; PROCEST; CENTRHODOPSN.
PROSITE; PSO0237; G_PROTEIN_RECEP_FI_1; 1.
PROSITE; PS50237; G_PROTEIN_RECEP_FI_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHEMOKINE RECEPTOR TYPE 7.
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EXTRACELLULAR (POTENTIAL).
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 2.6e-33; 67; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (POTENTIAL)
CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:103011; Cmkbr7.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42941 MW;
                                                                                                                                                                                                                                                                                                                                              EMBL; L31580; AAA74232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 140; Conservative
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378 AA;
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25
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DISULFID
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231 PNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTES 290
              2aballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
"Cutting edge: identification of the orphan chemokine receptor GPR-9-6
as CCR9, the receptor for the chemokine TECK.";
J. Immunol. 162:5671-5675(1999).
                                                                 FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
                                                   IALFHSCLNPILYVFMGASFKNYVMKVAKKYGSWRRQR-----QSVEFPFDSEGPTE
                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN LYMPH NODES AND SPLEEN.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 9 (C-C CKR-9) (CCR-9)
(Chemokine C-C receptor 10).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                     369 AA.
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InterPro; IPR004069; Chemokine9_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                    PRT;
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MEDLINE-99248139; PubMed-10229797;
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                                                                                                                                                                                                    STANDARD;
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85
106
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210
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254
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                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                      344 PTSTFS 349
                                                                                                                               372 TTTTFS 377
                                                                                                                                                                                                                                                                                           CCR9 OR CMKBR10.
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CKR9_MOUSE
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Best Local Similarity 36.5'
Matches 119; Conservative
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107
357 AA;
                                                                                GCRDb; GCR 1943;
MIM; 604738; -.
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O54689;
30-MAY-2000 (
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MEDLINE-99248139; PubMed=10229797;
MEDLINE-99248139; PubMed=10229797;
Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
Cutting edge: identification of the orphan chemokine receptor GPR-9-6
as CCR9, the receptor for the chemokine TECK.";
J. Immunol. 162:5671-5675(1999)
                                                                                                                                                                            67 AYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSG 126
                                                                                                                                                                                        MQFLACISIDRYVAVTKVPSQSGVGKPCW-----IICFCVWMAAILLSIPQLVFYT 177
                                                                                                                                                                                                                                        134 VLLIMCISVDRYIAIVQ-----AMKAQVWRQKRLLYSKMVCITIWVMAAVLCTPEILYSQ 188
                                                                                                                                                                                                                                                             234
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Receptor for chemokine SCVA25/TECK. Subsequently transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection. SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
                                                                                                                                                |: |: | ::| : | | ::| : | DESYDSTASTDDYMNLNFSSF--FCKKNNVRQFASHFLPPLYWLVFIVGTLGNSLVILVY 73
                                                                                                                                    10 DYYYEENEMNGTY----DYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                       OCT-1996 (Rel. 34, Created)
OCT-1996 (Rel. 34, Last sequence update)
ARR-2002 (Rel. 41, Last sequence to update)
chemokine receptor type 9 (C-C CKR-9) (CC-CKR-9) (GCR-9-
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-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLUNAC. . .) (POTENTIAL).
BY SIMILARIY.
W; 6971F76F0A24B4AE CRC64;
                                                                                                                                                                                                                                                            VNDN---ARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIK
                                                                                                                                                                                                                                                                                                     ISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Lautens L.L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.M.,
                                                                                           Length 369;
                                                                                     35.1%; Score 0.5,
36.0%; Pred. No. 1.2e-32;
+ive 77; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                     357 AA
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                                                                                                                Matches 118; Conservative
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255
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323
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01-0CT-1996
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P51686;
TRANSMEM
DOMAIN
TRANSMEM
                              DOMAIN
CARBOHYD
DISULFID
SEQUENCE
                                                                                            Query Match
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CKR9_HUMAN
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                               InterPro; IPR004069; Chemokine9_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
Fram; PF00101; 7m_1; 1.
PRINTS; PR0151; CHEMOKINE9.
PRINTS; PR01537; GPCRRHODOPSN.
PROSITE; PS02237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
G-PROFIE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
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7 (POTENTIAL).
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(Rel. 39, Last sequence update)
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62 VVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAV-NAVHGWVLGKIMCKITSALYT 120

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3 STESYFGTDD----YDNTEYYSIPPDHGPCSLEEVRNFTKVFVPIAYSLICVFGLLGNIM 58

121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCW----IICFCVWMAAILLSIPQLVF- 175

374 AA

STANDARD;

CKR6_HUMAN

RESULT 8 CKR6_HUMAN

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                                                                                                                                                                                                                  MEDLINE-99077268; PubMed-9862452;
Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
Albar J.P., Ardavin C., Marquez G.;
"Molecular cloning, functional characterization and mRNA expression
analysis of the murine chemokine receptor CCR6 and its specific ligand
                                                                                                                                                                                                                                                                                                           FEES Lett. 440:188-194(1998).

-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MID-3-ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEWEL.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
5-OCT-2001 (Rel. 40, Last annotation update)
-C chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (KY411).
                                                                 Cranlata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                          Yanagihara S., Komura E., Yamaguchi Y.;
"Mouse G protein-coupled receptor KY411.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00001; 7tm_1; 1.
PRINTS; PR01529; CHEMCKINER6.
PRINTS; PR00237; GPCRHODOSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR004067; Chemokine6_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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BY SIMILARIT
                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB009369; BAA23776.1; -. EMBL; AJ222714; CAA10956.1; -.
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                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 AA;
                                                                                            NCBI_TaxID=10090;
                                  CCR6 OR CMKBR6.
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JET FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCTUM IONS LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K., Nomiyama H., Yoshie O.:
"Identification of CCR6, the specific receptor for a novel
"Imphocyte-directed CC chemokine LARC.";
J. Biol. Chem. 272:14893-14898(1997).
P51684; 092846; P78553; 01-007-1996 (Rel. 34, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) 16-007-2001 (Rel. 40, Last annotation update) 16-007-2001 (Rel. 40, Last annotation update) 16-007-2001 (Rel. 40, Cast annotation update) 16-007-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97224503; PubWed=9070937; Liao F., Lee H.-H., Farber J.M.; "Cloning of STRL22, a new human gene encoding a G-protein-coupled receptor related to chemokine receptors and located on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.; "Molecular cloning and RNA expression of two new human chemokine
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Lautens L.L., Modi W., Bonner T.I.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCoy R., Perlmutter D.H.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 227:846-853(1996)
                                                                                                                                                                                                                                                        CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97313465; PubMed=9169459;
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8

26; Gaps

Score 605; DB 1; Length 367; Pred. No. 1.4e-30; Mismatches 125; Indels ;

:09

Conservative

Similarity

Query Match Best Local Simil Matches 129; C

ò

33.3%;

8 STDYYYEENEMNGTYDYSQYELI-----CIKEDVREFAKVFLPVFLTIVFVIGLAGNSM 61

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-i- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL LIVER EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN NATURAL KILLER CELLS, MONCYTES, OR GRANULOCYTES.
-i- INDUCTION: BY INTERLEDIXIN-2.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-i- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

G -> A (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                         A INTERPROJECTION ANAPHYLATOXIN.

InterPro; IPR000020; Anaphylatoxin.

InterPro; IPR000206; Chemokine6_receptor.

InterPro; IPR000206; Chemokine6_receptor.

InterPro; IPR000207; Chemokine6.

R Pfan; PF00001; 7tm 1; 1.

R PF1 PF00001; 7tm 1; 1.

R PROSITE; PS00237; G_PROFIN_RECEP_F1_1; 1.

R PROSITE; PS00237; G_PROFIN_RECEP_F1_2; 1.

R PROSITE; PS00237; G_PROFIN_RECEP_F1_2; 1.

TRANSHEM 48 74 IQPOTENTIAL).

T TRANSHEM 48 74 IQPOTENTIAL).

T TRANSHEM 84 104 2 (POTENTIAL).

T TRANSHEM 84 104 2 (POTENTIAL).

T DOMAIN 105 119 EXTRACELULAR (POTENTIAL).

T DOMAIN 105 119 EXTRACELULAR (POTENTIAL).
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D7F963534E990BC4 CRC64;
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5 (POTENTIAL).
6 (POTENTIAL).
EXTRACELLUIAN (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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7 -> V (IN REF. 4).
8 -> T (IN REF. 5).
7 -> S (IN REF. 5).
9 -> L (IN REF. 4).
9 -> C (IN REF. 4).
1 -> F (IN REF. 4).
1 -> F (IN REF. 4).
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                                                                                                                                                                                                             EMBL; U45984; AAB62714.1; -.
EMBL; Z79784; CAB02144.1; ALT_INIT.
EMBL; U60000; AAB06949.1; -.
EMBL; U68030; AAC51124.1; -.
EMBL; U68032; AAC51125.1; -.
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GCRDb; GCR_1037; --
GCRDb; GCR_1076; --
GCRDb; GCR_1906; --
GCRDb; GCR_1919; --
GCRDb; GCR_1911; --
GCRDb; GCR_21911; --
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206
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374 AA;
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                                                                     YYKKQRTKTDVYILNLAVADLLLLFTLPFWAV-NAVHGWVLGKIMCKITSALYTLNFVSG 126
                                                                                                                   MQFLACISIDRYVAVTKVPS----QSGVGKPCWIICFCVWMAAILLSIPQLVF---YTVN 179
                                                                                                                                                                                    180 DNARCIPIFPRYLGTS----MKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKI 235
                                                                                                                                                                                                                                                         236 SRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFH 295
                                                                                                                                                                                                                                                                                        250 HKAIRVIIAVVLVFLACQIPHNMVLLVTAAN-LGKMNRSCQSEKLIGYTKTVTEVLAFLH 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 6 (CXC-R6) (G protein-coupled
Nature 388:296-300(1997).
-1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCLJ6. USED AS A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
-1- SUBCELLUIAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopitheous acthiops (Green monkey) (Grivet).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Cercopithecidae;
Cercopithecinae, Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.; "Expression cloning of new receptors used by simian and human immunodeficiency viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCRDb; ACC. 211; -. GCRD. TRHOdpsn.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHHODDSN.
PROSITE; PS020237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
32 EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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MEDLINE-97373958; Pubmed-9230441;
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O18983;
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CCR6_CERAE
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Score 583; DB 1; Length 374; Pred. No. 3.2e-29; 68; Mismatches 120; Indels

32.1%; 36.1%;

Best Local Similarity 36.18 Matches 121; Conservative

Query Match

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15-JUL-1998 (Rel. 36, Last seq
01-MAR-2002 (Rel. 41, Last anno
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CXCR6 OR BONZO.
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CCR6_MACNE
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                                                                                                                                                                                                                                                                 CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPQLVFYTV--NDNARCI 185
                                                                                                                                                                                                                                                    72 QRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 6 (CXC-R6) (CXCR-6) (G protein-coupled caceptor bonzo) (G protein-coupled receptor STRL33).
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                    HYEDNGFNSFNDSSQEE----HQDFLQFSKVFLPCMYLVVFVCGLVGNSLVLVISIFYHK 61
                                                                                                                                                                                                         12 YYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIDS RES. Hum. Retroviruses 17:981-986(2001).
-1- FUNCTION: RECEPTOR FOR THE C.*C CHEMOKINE CXCL16. USED AS A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                             186 PIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTV
                                                                                                                                                                                                                                                                                                                                                                 ----GYHDEEISTVVLATQMTLGFFLPLLAMIVCYSVIIKTLLHAGGFQKHRSLKIIFLV
                                                                                                                                                                                                                                                                                                                                                                                      VIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Margulies B.J., Hauer D.A., Clements J.E.; Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                             LINKED (GLCNAC. . .) (POTENTIAL).
6CBFE389C6E5919E CRC64;
                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 VSLKFRKNFWKLVKDIGCLPYLGVSHQWKSSEDNSK--TFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                   MGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSIFSI 350
                                                                                                                                                         31.9%; Score 581; DB 1; Length 342; 34.2%; Pred. No. 3.9e-29; 1ve 71; Mismatches 130; Indels
         4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
                                                                                                    SIMILARITY
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                                                                                                                          39226
                                                                                                                                                                                  Conservative
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                                                      259
275
293
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                                                                                                                                                                      Similarity
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                                                                                                                          342
                                                                                                                                                            Query Match
Best Local Simi
Matches 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 KKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LTCITVDRFIVVVKATKAYNQQAKRMTWGKVICLLIWVISLLVSLPQIIYGNVFNLDKLI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 DYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LACISIDRYVAVTKVPS -- QSGVGKPCW -- IICFCVWMAAILLSIPQLVFYTV -- NDNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIPIFPRYLGTSMKALIOMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 C----GYHDEEISTVVLATOMTLGFFLPLLAMIVCYSVIIKTLLHAGGFQKHRSLKIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 TVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 VFMGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca nemestrina (Pig-tailed macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73; Mismatches 132; Indels
                                                                                                                             EMBL, AF124380; AAD31419.1; -.
InterPro; IrROD376; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1: 1.
PRINTS: PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2: 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Last annotation update)
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237 MAVFLLTQTPFNLVKLIRSTHWEYYAMTSFHYT-----IIVTEAIAYLRACLNPVLYAF 290
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PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Blood;
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                                                                                       RESULT 12
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                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPQLVFYTV--NDNARCI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 PIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GYHDKEISTVVLATQMTLGFFLPLLAMIVCYSVIIKTLLHAGGFQKHRSLKIIFLV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 VIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILIVF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 ORTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 YYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKK 71
                                                                                                                        -I FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
-I SUBCELLUIAR LOCATION: Integral membrane protein COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 CITVDRFIVVVKATKAYNQOAKRMTWGKVICLLIWVISLLVSLPQIIYGNVFNLDKLIC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                 SEQUENCE FROM N.A. MEDINE-9737958; PubMed-9230441; MEDINE-9737958; PubMed-9230441; Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.; Expression cloning of new receptors used by simian and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 342;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.3%; Score 569; DB 1; Length 34
33.6%; Pred. No. 2.1e-28;
tive 72; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                               Pfam; PF00001; /tm_i; GPCRHDODSN.
PRINTS; PR00237; GPCRHDODSN.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
32 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                         1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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55F9F68CB62D2DF5 CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                            EMBL; AF007858; AAB64224.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 1
39297 MW;
                                                                                                   immunodeficiency viruses.";
Nature 388:296-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.3'
Best Local Similarity 33.6'
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164
187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294
102
16
342 AA;
                         NCBI_TaxID=9545;
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TRANSMEM
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DOMAIN
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SEQUENCE
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000574, 000575,
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
02-X-C chemokine receptor type 6 (CXC-R6) (CXCR-6) (G protein-coupled receptor bonzo) (G protein-coupled receptor STRL33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "STRL33, A novel chemokine receptor-like protein, functions as a fluston cofactor for both macrophage-tropic and T cell line-tropic HIV-1.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
---SWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                        VSLKFRKNFWKLVKDIGCLPYLGVSHOWKSSEDNSK -- TFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97373958; PubMed-9230441;
Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
"Expression cloning of new receptors used by simian and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liao F., Alkhatib G., Peden K.W.C., Sharma G., Berger E.A., Farber J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Exp. Med. 185:2015-2023(1997).
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306 MGASFKNYVMKVAKKYG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, Y13248; CAA73698.1; -. GCRDb, GCR_1328; -. GCRDb; GCR_1330; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunodeficiency viruses.";
Nature 388:296-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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8
G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Glycoprotein; Polymorphism.
32 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 LQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLILT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPQLVFYTV--NDNARCI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 ORTKTBVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 YYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 YHEDYGFSSFNDSSQEE----HQDFLQFSKVFLPCMYLVVFVGGLVGNSLVLVISIFYHK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKR4_HUMAN STANDARD; PRT; 360 AA.
P51679; Q9ULY6; Q9ULY7;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
C-C_Chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 PIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ----GYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 VIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILIVF
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                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
D -> A (IN STRL33.3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 MGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSI 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 VSLKFRRNFWKLVKDIGCLPYLGVSHQWKSSEDNSK--TFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEQUENCE FROM N.A.
TISSUE-Spleen;
MEDLINE-95370289; Pubwed-7642634;
Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                     3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                             1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9FBC025556D1082E CRC64;
                                                                                                                                                                                                                                                                             5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 560; DB 1;
Pred. No. 7.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    003506
                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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59
68
68
103
1125
1143
125
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180
160
160
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90
104
1126
1144
1165
1188
232
232
232
232
102
102
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Matches 117;
    PROSITE; I
                                                    G-protein
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TRANSMEM
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                                                                                                           SECUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
MEDLINE=21040311; PubMed=11196669;
Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
Hirai K., Tokunnaga K.,
"New variations of human Cc-chemokine receptors CCR3 and CCR4.";
Genes Immun. 1:97-104(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemokine, and 1-309.";
J. Immunol. 164:4048-4054(2000)

1. Immunol. 164:4048-4054(2000)

1. FUNCTION: HIGH AFFINITY RECEPTOR FOR THE C-C TYPE CHEMOKINES

TRAC/SCYA17 AND MOC/SCYA22. THE ACTIVITY OF THIS RECEPTOR IS

MEDIATED BY G(1) PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM. CAN FUNCTION AS A CHEMOATTRACTANT
HOMING RECEPTOR ON CIRCULATING MEMORY LYMPHOCYTES AND AS A
CORECEPTOR FOR SOME PRIMARY HIV-2 ISOLATES. IN THE CNS, COULD
MEDIATE HIPPOCAMAL.NEURON SURVIVAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Imai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,
Yoshie O., Gray P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIATE HISTOLANTAL RELEAR.

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE THYMUS, IN
PERIPHERAL BLOOD LEUKOCYTES, INCLUDING T CELLS, WOSTLY COR4 CELLS,
AND BASOPHILS, AND IN PLATELETS; AT LOWER LEVELS, IN THE SPLEEN
AND IN MONOCYTES. DETECTED ALSO IN MACNOPHAGES, IL-2-ACTIVATED
NATURAL KILLER CELLS AND SKIN-HOMING MENORY T CELLS, MOSTLY THE
ONES EXPRESSING THE CUTANBOUS LYMPHOCYTE ANTIGEN (CLA). EXPRESSED
IN BRAIN MICROVASCULAR AND CORONARY ARTERY ENDOTHELIAL CELLS.
PTM: IN NATURAL KILLER CELLS, SCYAZD BINDING INDUCES
PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
BY BETA-ADRENERGIC RECEPTOR KINASES I AND 2.

SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P., Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher B.C., "The chemokine receptor CCR4 in vascular recognition by cutaneous but not intestinal memory T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ဌ
                               novel CC chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20219238; PubMed-10754297; Inngjerdingen M., Damaj B., Maghazachi A.A.; "Human NK cells express CC chemokine receptors 4 and 8 and respond thymus and activation regulated chemokine, macrophage-derived
                                                                                                                                                                                                                                                                                                                           Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.; The T cell-directed CC chemokine TARC is a highly specific biological ligand for CC chemokine receptor 4."; J. Biol. Chem. 272:15036-15042(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Macrophage-derived chemokine is a functional ligand for the CC chemokine receptor 4.";
                      "Molecular cloning and functional expression of a receptor cDNA from a human basophilic cell line."; J. Biol. Chem. 270:19495-19500(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            emokine receptor 4.";
Biol. Chem. 273:1764-1768(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99394604; PubMed=10466728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98104168; PubMed=9430724;
                                                                                                                                                                                                                                                                                                       MEDLINE=97313486; PubMed=9169480;
Proudfoot A.E.I., Wells T.N.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X85740; CAA59743.1; -.
EMBL; AB023888; BAA86965.1; -.
EMBL; AB023889; BAA86966.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 400:776-780(1999).
                                                                                                                                                                                                                                                                               FUNCTION
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1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
                                                                                                                                                                                                                                                                                                                                                                                                  Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
         High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (GRO/MGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DATABASE: NAME-PROW; NOTE-CD guide CDw128b entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdw128b.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular characterization of receptors for human interleukin-8, {\rm GRO/melanoma} growth-stimulatory activity and neutrophil activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Placenta;
MEDLINE-95014476; PubMed-7929358;
Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
Comparison of the genomic organization and promoter function for human interleukin-8 receptors A and B.";
J. Biol. Chem. 269:26381-26389(1994).
                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sprenger H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.; "Structure, genomic organization, and expression of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92355587; PubMed-1379593;
Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wor
"Characterization of two high affinity human interleukin-8
                                                                                                                                                                                                                                  Murphy P.M., Tiffany H.L.; "Cloning of complementary DNA encoding a functional human
                          receptor) (IL-8 receptor type 2) (CDW128b).
IL8RB OR CXCR2.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE-93205012; PubMed-8384312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure, genomic organization, and
interleukin-8 receptor B gene.";
J. Biol. Chem. 269:11065-11072(1994).
                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91368200; Pubmed=1891716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94209273; PubMed-7512557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Immunol. 30:359-367(1993).
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EMBL; M94812; AAC14460.1; --
EMBL; L19593; AAB59437.1; --
EMBL; U11869; AAB60656.1; --
                                                                                                                                                                                                                                                                                interleukin-8 receptor.";
Science 253:1280-1283(1991).
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PIR; A53611; A53611.
HSSP; P34996; 1DDD.
GCRDb; GCR_0077; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide-2.
         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 KKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 KRLRSWIDVYLLNLAISDLIFVFSLPFWGYYAADQWVFGLGLCKMISWWYLVGFYSGIFF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 LACISIDRYVAVTKV----PSQSGVGKPCWIICFCVWMAAILLSIPQLVF---YTVN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 VMLMSIDRYLAIVHAVFSLRARTLTYGV----ITSLATWSVAVFASLPGFLFSTCYTER 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNARCIPIFPRYLGTSMKALIQMLEI-CIGFVVPFLIMGVCYFITARTLMKMPNIKISRP 238
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7 (POTENTIAL).
CYTODIASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                           InterPro: IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS: PR00237; GPCRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Phosphorylation; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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51EBE12AD1FAFABF CRC64;
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CYTOPLASMIC (POTENTIAL).
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6 (POTENTIAL).
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(Rel. 33, Last sequ
(Rel. 40, Last anno
  EMBL; AB023890; BAA86967.1; -. EMBL; AB023891; BAA86968.1; -. EMBL; AB023892; BAA86969.1; -.
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BAA86967.1; -
BAA86968.1; -
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Best Local Similarity 35.8
Matches 115; Conservative
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268
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P25025;
01-MAY-1992 (
01-FEB-1996 (
16-OCT-2001 (
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IL8B_HUMAN
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353
353 AA;
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                                           NCBI_TaxID=9598;
            LEBRB OR CXCR2
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                                                                                                                                                                                                                                                                                                                                                               58 GNSMVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSA 117
                                                                                                                                                                                                                                                                                                                                  238
                                                                                                                                                                                                                                                                                                                                                                                                                    228 MKMPNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQV 287
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                                                                                                                                                                                                                                                                                                                                                                                     175 F----YTVNDNARCIPIFPRYLG---TSMKALIQMLEICIGFVVPFLIMGVCYFITARTL
                                                                                                                                                                                                                                                                                                                                                                                                  183 FRRTVYSSNVSPACY----EDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                   239 FKAHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDA
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                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                            29.4%; Score 534.5; DB 1; Length 360; 33.2%; Pred. No. 2.8e-26; tive 75; Mismatches 141; Indels 25
                                                            PRINTS; PR00237; GFCRRHODOPSN.
PROSTTE; PS00237; G_ROTHIN_RECEP_F1_1; 1.
PR051TE; PS00237; G_ROTHIN_RECEP_F1_2; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                   EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                       6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                              SIMILARITY.
564F04A8BCCOA197 CRC64;
                                                                                                            1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
                                                                                                                                          3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Last annotation update)
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                                    InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000832; GPCR_secretin.
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                                                    PF00001; 7tm_1; 1
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183
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120
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(Rel. 35,
(Rel. 35,
                      GCR_1831; -.
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22
119
360 AA;
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      GCR_1001;
GCR_1339;
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76
85
106
1121
1143
1164
1184
                              MIM; 146928;
                                                                                           Chemotaxis.
                                                                                                                                                                                                                                                                           120;
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01-NOV-1997
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Q28807;
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TRANSMEM
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Best Local S
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              GCRDb;
                       3CRDb;
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Matches
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IL8B_PANTR
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                                                                                                                                                                                                                                                                               LOPGZ-Larrea C.;

"Characterization of interleukin-8 receptors in non-human primates.";

"Characterization of interleukin-8 receptors in non-human primates.";

Immunogenetics 43:261-267(1996).

Immunogenetics 43:261-267(1996).

INTERLEUKIN-8, WHICH IS A POWERFUL

NEUTROPHILS. THIS RECEPTOR

GAUSES ACTIVATION OF NEUTROPHILS. THIS RESONOSE IS MEDIATED VIA A

G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSTYOL-CALCIUM SECOND

MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY

AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 GNSMVVAIYAYYKKQRTKTDVYILNLAVADLLLETLPFWAVNAVHGWVLGKIMCKITSA 117
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                                                                                              Euteleostomi;
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                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
MEDLINE=96175151; PubMed=9110929;
ALVAIEZ V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                   Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis; cell proliferation; anti-inflammatory; anti-anglogenic; antitumor; HIV; anti-allergic; antiviral.
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AAM99949
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  WPI; 1999-620375/53.
N-PSDB; AAZ90528.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AAY94325
AAG80119
AAU08994
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AAB62389
AAW93170
AAY30125
AAY71301

    protein search, using sw model

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New nucleic acid encoding human BGCKr receptor, used e.g. for modulating inflammation and tumor growth $\,$

Human orphan G pro

Score

Result Š

7TM receptor prote Human CCR9a protei Epstein Barr virus G-protein coupled

Novel human diagno Putative seven tra Human mutant G pro

Human G protein-co

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represents the full-length human BGCKr protein
                                                                                                                                                                                                                                                                                                            Human signal peptide-containing protein SP-16.
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    Fig 2A-B; 123pp; English.
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                                                                                                           Similarity
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treatment; F14041 protein; gene therapy; immune response; vaccine; HIV-2; incollate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer; diabetes; anorexia; bullimia; Parkinson's disease; acute heart failure; hypotension; hypertension; uninary retention; osteoporosis; allergy; angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia; anxiety; manic depression; delirium; dementia; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; linkage analysis; gene mapping; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HFIA041; G-coupled receptor; disease susceptibility; diagnosis; immunise;
                                                                                                                                                                        The present sequence represents a human signal peptide-containing protein (SP), designated SP-16. SP proteins can be used to stimulate cell proliferation or to treat or prevent cancer. SP antagonists are also used to treat or prevent cancer, and also for treating or preventing neuronal disorders or immune responses. Polynucleotide sequences complementary to the SP-encoding polynucleotides are useful for the detection of SP-encoding nucleic acid molecules in biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 MVVAIYAYYKKORTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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Mathur P,
                                                                                                                                        Claim 1; Fig 1; 83pp; English.
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                                                        The invention relates to a human BGCKr protein, a G-protein coupled receptor. The BGCKr protein can be expressed by standard recombinant methodology. BGCKr are receptor proteins possibly involved in modulation of proinflammatory or stimulatory functions of chemokines; cell proliferation, migration, adhesion and targeting, and excoytosis. The BGCKr nucleic caids and derived proteins (or their variants), antibodies and modulators are potentially useful for modulating inflammation; chemoattractant activity of leucocytes; angiogenesis; cell proliferation; tumour growth; allegic reactions and entry of human immune deficiency virus into cells, for therapeutic or prophylactic purposes. They are also used for diagnosis and in drug-screening assays. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signal peptide-containing protein; SP; cell proliferation; neuronal disorder; immune response; detection.
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                                                                                                                                                                                                                                                                                                                                                                                      Length 350;
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100.0%; Pred. No. 1.6e-195;
iive 0; Mismatches 0; I
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Gaps

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Indels

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5.0kb species. VSHK-1 polynucleotides can be used as hybridisation probes
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                                                                                                                                                                                             AAY94325;
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                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a G-coupled receptor, HFIAO41 which is useful for diagnosing susceptibility to diseases by detecting mutations in the HFIAO41 gene, and can diagnose diseases associated with HFIAO41 protein imbalance by determining HFIAO41 polypeptide expression levels, Agonists and antagonists of the protein can be used in treatment to activate (agonist) or inhibit (antagonist) HFIAO41 activity, in addition to direct administration of antisense sequences to prevent expression, or HFIAO41 colymportide expression. HFIAO41 activity, in addition to direct administration of antisense sequences to prevent expression, or HFIAO41 colymportide expression. HFIAO41 antiboddes are useful for inducing an immune response to immunise and prevent disease, and for isolating topolypeptide sor purifying the polypeptides by affinity chromatography. HFIAO41 clones or purifying the polypeptides by affinity chromatography. HFIAO41 polypeptides can be administered directly or as a vaccine to include bacterial, fungal, protozoan and viral infections, particularly HIV-1 or -2 infections; cancer; diabetes; anorexia; builmia; parkinson's disease; acute heart failure; hypocression; hypertension; urinary cretention; osteoporosis; angina pectoris; myocardial infarction; acteoporosis; angina pectoris; myocardial infarction and dyskinesias asthm as allergies; benign prostatic hypertrophy; and psychotic and neurological disorders, including anxiety, schizophrenia, manic neurological disorders, including anxiety, schizophrenia, and dyskinesias such as Huntington's disease or Gilles de la Tourette's syndrome. The HFIAO41 polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240
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                                                                                                                                                                                                                                                                                                        New G-coupled receptor (HFIAO41) polypeptide and polynucleotide -
useful as diagnostic reagents and for prevention and treatment of
cancer, HIV infections and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 22-23; 27pp; English.
                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                            97US-0962922.
97US-0055895.
                                                                          98EP-0301170.
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Best Local Similarity 100.
Matches 350; Conservative
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                                                                                                                                                                                                                                                                   N-PSDB; AAX22557
                                                                          17-FEB-1998;
                                                                                                                27-OCT-1997;
                                                                                                                                  15-AUG-1997;
EP899332-A2
                                    03-MAR-1999
                                                                                                                                                                                                             Ellis CE;
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The present sequence is VSHK-1, a new seven transmembrane receptor which contains seven membrane-spanning helical domains that are linked by three intracellular and three extracellular loops. The gene sequence encoding VSHK-1 was isolated from a cDNA library. In heart tissue, where VSHK-1 is predominantly found, three RNA species were identified: a 1.3kb; a 2.0kb; and a 5.0kb species. The polynucleotide encoding the present sequence corresponds to the 2.0kb form. The 1.3kb form may result from the use of an alternative polyadenylation site while transcription of a 3.0kb intron at nucleotide 74 could account for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polypeptide comprising a new seven-transmembrane receptor protein and its encoding polynucleotide, useful for the analysis of {\sf VSHK-1} -
                                                                                                                                                                                                                                                                                                                                                                                                Human; seven transmembrane receptor; VSHK-1; signal transduction.
"potential N-glycosylation site"
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/label- Transmembrane_domain
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/label= Transmembrane_domain
276..278
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                                                                                                                                                                                                                                                                                                                                            Human seven transmembrane receptor VSHK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                      AAY94325 standard; Protein; 350
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99US-0114856
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/label- Tr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAY94325
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06-JAN-1999;
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to detect and measure VSHK-1 mRNA. They may also be used to identify substances that modulate the level of VSHK-1 mRNA. The VSHK-1 coding sequence can be integrated into an expression vector for production of VSHK-1 receptor polypeptides in host cells. The polypeptides can be used to identify agents which modulate VSHK-1 receptor signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                        180
                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnostic agent containing two or more receptor-specific ligands,
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                                                                                                                                                                      NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK
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                                                                                                                Length 350;
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                                                                                                               Score 1819; DB 21;
Pred. No. 1.6e-195;
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                                                                                                                                      Mismatches
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                                                                                                                                      o;
                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IPFP-) IPF PHARM GMBH. (FORS/) FORSSMANN U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CCR11 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-626256/72.
                                                                                                                            Similarity
                                                                                 350 AA;
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                                                                                                                 Query Match
Best Local Simi
Matches 350;
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                                                           activity
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                                                                                                                                        Also introduction, organ rejection, inflammation and autoimmune diseases.
Also inhibitors of (I) are used the rapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), where the (cardio)vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiasthmatic, immunosuppressive, dermatological, antirheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. AdG80045-AAG80128 represent human chemokine fragments used to illustrate the method of the invention.
                                                                                           This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal
for detecting tumors, inflammation etc., also therapeutic use of inhibitors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiatherosclerotic; analgesic; cytostatic; antianginal; cardiovascular disorder; angiogenesis-related disorder; neural disorder; pain response disorder; inflammatory disorder; atherosclerosis; angina pectoris; myocardial infarction; ischaemic heart disease; sudden cardiac death; obesity; hypertensive heart disease; diabetes; prostate cancer-related pain.
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                                                             German
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                                                           Page 11; 26pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 350; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     350 AA;
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                                                               Disclosure;
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Homo sapiens

Key Region

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Human; chemokine receptor; CCRII; G protein coupled receptor; inflammatory bowel disease; asthma: angiogenesis; artherosclerosis vascular association disease; hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon; left ventricular distolic dysfunction; migraine; preterm labour; oesophageal spasm; ischaemic stroke; subbarachnoid haemorrhage; myocardial infarction; congestive heart failure; endometriosis; vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the human chemokine receptor CCRII. CCRII is a member of the G protein coupled receptor family. A CCRII polypeptide, its inhibitor, an antibody, or other modulator of CCRII expression or biological activity, is useful for treating many inflammatory diseases, for example, rheumatoid arthritis, inflammatory bowel disease, and astima. They are also useful for treating any angiogenesis, artherosclerosis vascular association diseases which may include but are not limited to hypertension, angina pectoris, cardiac arrhythmias, left ventricular diastolic dysfunction, Raynaud's phenomenon, migraine, preterm labour, oscophageal spasm, ischaemic stroke, subarachnoid haemotrhage, myocardial infarction, congestive heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated polynucleotide encoding the chemokine receptor CCRII, useful for treating rheumatoid arthritis, inflammatory bowel disease, asthma, angiogenesis, artherosclerosis, cardiac arrhythmias, Raynaud's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240
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                                       of human chemokine receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 96-97; 110pp; English.
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Conservative
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(first entry)
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                                         acid sequence
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                                                                                                                                                                                                                                                                        Homo sapiens.
13-NOV-2001
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Matches 350;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Novel G protein coupled receptors and nucleic acids encoding them, for identifying agents for the treatment of cardiac disorders
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125..141
/label- G_protein_receptor_signature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Fig 9; 209pp; English.
                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                   28-FEB-2001; 2001WO-US06543
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Best Local Simi
Matches 350;
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HFIAO41; G-coupled receptor; disease susceptibility; diagnosis; immunise; treatment; FIAO41 protein; gene therapy; immune response; vaccine; HIV-2; incoulate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer; diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure; hypotension; hypertension; urliary retention; osteoporosis; allergy; angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia; ansiety; manic depression; delirium; dementia; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; linkage analysis; gene mapping; human; ss.
                                                                                                                                                                                                                                                                                                                           61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                                                      Score 1819; DB 22;
Pred. No. 1.8e-195;
Mismatches 0;
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100.0%;
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97US-0055895.
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                                                                                     Similarity
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                                                            Match
                                                            Query Match
Best Local
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narcipifprylgtsmkaliqmleicigfvvpflimgvcyfitartlmkmpnikisrplk 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemokine receptor; CCX CKR; chemokine; ELC; SLC; TECK; modulator; antinflammatory; immunosuppressive; cytostatic; antiallergic; human; immunostimulant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schall TJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "encoded by TAA"
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                                                                                                                                                                                                                                                                                                                                                                                  AAB62389 standard; Protein; 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Fig 1; 72pp; English.
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99US-0159210.
99US-0172979.
99US-0173389.
2000US-0186626.
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20-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB62389;
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polynucleotide - and treatment of

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Human; orphan G protein-coupled receptor; GPCR; hPPR1; drug screening; transmembrane receptor; expressed sequence tag; EST; signal cascade.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a seven-pass transmembrane receptor protein. The protein and its DNA can be used to screen substances for the diagnosis, prevention and treatment of autoimmune diseases, particularly those due to white blood call dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS
                                                                                                                                                                                                                                                                                                                                                                New seven-pass transmembrane receptor protein useful for treating, preventing or diagnosing autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1814; DB 20;
Pred. No. 5.8e-195;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human orphan G protein-coupled receptor hPPR1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 101-103; 118pp; Japanese.
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                                                                                                                                                                                                                                                         Ohno T;
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Best Local Similarity
Matches 349; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 AA;
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Homo sapiens.
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                                                                                                                           24-DEC-1998;
                                                                                                                                                                                                                                                      Ishimaru H,
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                                               This sequence encodes a G-coupled receptor, HFIA041 which is useful for diagnosing susceptibility to diseases by detecting mutations in the HFIA041 gene, and can diagnose diseases associated with HFIA041 protein imbalance by determining HFIA041 polypeptide expression levels, Agonists and antagonists of the protein can be used in treatment to activate (agonist) or inhibit (antagonist) HFIA041 activity, in addition to direct administration of antisease sequences to prevent expression, or HFIA041 conditions associated with a lack of FIA041 polypeptide expression. HFIA041 antibodies are useful for inducing an immune response to immunise and prevent disease, and for isolating immune response to immunise and prevent disease, and for isolating continuate against disease. Diseases diagnosed, prevented and treated includes bacterial, fundal, protozoan and viral infections, particularly HTA041 polypeptides by affinity chromatography. HTA041 polypeptides can be administered directly or as a vaccine to include bacterial, fundal, protozoan and viral infections, particularly HTA041 or -2 infections; cancer; diabetes; anorexia; bullmia; particularly HTV-1 or -2 infections; cancer; diabetes; anorexia; bullmia; particularly HTV-1 or -2 infections; cancer; diabetes; anorexia; bullmia; particularly cremention; cateoporosis; angina pectoris; myocardial infarction; ulcers; asthma; allergies; benign prostatic hypertrophy; and psychotic and neurological disorders, including anxiety, schizophrenia, manic cepromosis, disease or Gilles de la Tourette's syndrome. The HTA041 polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis.
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100.0%; Pred. No. 5.8e-195;
ive 0; Mismatches 0;
                 Page 25-26; 27pp; English.
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WPI; 2000-317986/27.
N-PSDB; AAA46029.
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03-SEP-1999;
29-SEP-1999;
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28-MAY-19
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12-MAR-1
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                                                                                                                                                                                                                                                                                                                                                                            Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         Claim 42; Page 69-70; 102pp; English
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                                                                                     99US-0121852.
99US-0123946.
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99US-0157282
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                                               99WO-US23687
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es 348; Conserv
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        WO200031258-A2
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28-MAY-1999)
28-MAY-1999)
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29-SEP-1999;
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01-0CT-1999;
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01-0CT-1999;
01-0CT-1999;
                                                                  20-NOV-1998;
16-FEB-1999;
26-FEB-1999;
                                               13-OCT-1999;
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Matches
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NARCIPIFPRYLGTSMKALIOMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK
                                                                                                                                                                                                                                                                                                                                                                                                               Human; G protein coupled receptor; GPCR; transmembrane receptor; identification; agonist; screening; therapeutic; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dang HT;
                                                                                                                                                                                                                                                                                                                                                                                 Human G protein coupled receptor hPPR1 protein SEQ ID NO:24
                                                                                                                                                                                                  301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lehmann-Bruinsma K, Chalmers DT, C
law CW, Lin I, Lowitz K, White C;
                                                                                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                                                                                             AAB02835 standard; Protein; 350
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99US-0136436.
99US-0136437.
99US-0137127.
99US-0137131.
99US-0137131.
99US-0141448.
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98US-0109213.
98US-0110060.
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99US-0121852.
99US-0123944.
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99US-0123946.
99US-0123948.
99US-0123949.
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99US-0156633.
99US-0156555.
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                                                                             The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46617 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; TSC; tuberous sclerosis complex; cytostatic; antimicrobial; osteopathic; antialsthmatic; antiallergic; neuroprotective; cardiant; hypotensive; hypertensive; noctropic; anticonvulsant; analgesic; tranquiliser; immunosuppressive; antinflammatory; gene therapy; TSC7; infection; cancer; autoimmune disorder; Parkinson's disease; osteoporosis; neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                   receptor, inverse or partial agonists useful as therapeutic agents
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Non-endogenous, human G protein-coupled receptors for screening
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Pred. No. 1.6e-194;
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                                                Example 1; Page 99-100; 187pp; English.
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99.4%;
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Matches 348; Conservative
                                                                                                                                                                                                                                                    350 AA;
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                                                                                                                                                                                                                                                                                                 Query Match
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The present sequence is human tuberous sclerosis complex 7 (TSC7).

TSC7 polynucleotides and polypeptides are useful for determining the presence or predisposition to a disease associated with altered levels of TSC7. TSC7 polynucleotides, polypeptides and antibodies specific for the polypeptide are useful for treating or preventing pathological conditions associated with the disorder in a G-protein mediated pathway. They are useful for diagnosing a hyperproliferative condition such as a neoplasm or dermatological condition. TSC7 nucleic acids and polypeptides are useful in the treatment of microbial infections, pain, cancer, anorexia, asthma, autoimmune disorders, parkinson's disease, autothe hart failure, hypo/hypertension, osteoporosis, multiple sclerosis, angina pectoris, myocardial infarction, ulcers, allergies, benign prostatic hypertrophy and neurological disorders, including schizophrenia, dementia, severe mental retardation and dyskinesias, such as the funtington's disease and/or other pathologies and disorders TSC7 polypeptides are also useful as immunogens to produce antibodies and as
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                                                                                                                                                   Novel nucleic acid encoding G-protein coupled receptor for diagnosis and treatment of conditions associated with disorder in a G-protein mediated pathway such as cancer, neurological disorders and infections
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Pred. No. 2.7e-194;
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20-APR-2000; 2000US-0556002
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Matches 348; Conservative
                                 (CURA-) CURAGEN CORP
                                                                                                  2000-679670/66
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Best Local Similarity
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                                                                  Gould-Rothberg BE;
                                                                                                                  N-PSDB; AAC68722
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The invention relates to a human BGCKr protein, a G-protein coupled receptor. The BGCKr protein can be expressed by standard recombinant methodology. BGCKr are receptor proteins possibly involved in modulation of proinflammatory or stimulatory functions of chemokines; cell proliferation, migration, adhesion and targeting, and exocytosis. The BGCKr nucleic acids and derived proteins (or their variants), antibodies and modulators are potentially useful for modulating inflammation; tumour growth; altergic reactions and entry of human immune deficiency virus into cells, for therapeutic or prophylactic purposes. They are also used for diagnosis and in drug-screening assays. The present sequence represents the sequence of a partial human BGCKr protein.
                                    BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis; cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV; anti-allergic; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 ivkfcraidiiyslitscnmskrmdiaiqvtesialfhsclnpilyvfmgasfknyvmkv 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 333;
                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding human BGCKr receptor, used e.g.
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                                                                                                                                                                                                                                                                                                                                                                                             modulating inflammation and tumor growth
            Human BGCKr partial amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1A-B; 123pp; English.
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                                                                                                                                                                                                                                                                                                     Gonzalo JA, Gutierrez-Ramos
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                                                                                                                                                                                                                                                                        (MILL-) MILLENIUM PHARM INC
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Matches 333; Conservative
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                                                                                                         Homo sapiens
                                                                                                                                     WO9952945-A2
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16-APR-1999;
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                                                                                                                                             Human; chemokine receptor; CCR11; G protein coupled receptor; inflammatory disease; archamatoid arthritis; inflammatory bowel disease; asthma; angiogenesis; artherosclerosis vascular association disease; hypertension; angina pectoris; cardiac arrhythmia; Raymaud's phenomenon; left ventricular disscolic dysfunction; migraine; preterm labour; oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage; myocardial infarction; congestive heart failure; endometriosis; vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the bovine chemokine receptor CCRII. CCRII is a member of the G protein coupled receptor family. A CCRII polypeptide, its inhibitor, an antibody, or other modulator of CCRII expression or biological activity, is useful for treating many inflammatory diseases, for example, rheumatoid arthritis, inflammatory bowel disease, and asthma. They are also useful for treating many angiogenesis, artherosclerosis vascular association diseases which may include but are not limited to hypertension, angina pectoris, cardiac arrhythmias, left ventricular diastolic dysfunction, Raynaud's phenomenon, migraine, preterm labour, oesophageal spasm, ischaever beart failure, endometriosis, vascospasm, retinopathy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An isolated polynucleotide encoding the chemokine receptor CCRII, useful for treating rheumatoid arthritis, inflammatory bowel disease, asthma, angiogenesis, artherosclerosis, cardiac arrhythmias, Raynaud's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 MYVAIYAYYKKQFTKTDVXILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steiner B;
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                                                                                                                Amino acid sequence of bovine chemokine receptor CCR11.
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86.0%; Pred. No. 3.5e-173;
iive 27; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Epp A, Raport CJ,
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              AAG67238 standard; Protein; 350 AA.
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2000US-0187231
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                                                                                   (first entry)
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03-MAR-2000;
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Gaps

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Search completed: August 6, 2002, 18:08:09 Job time: 629 sec

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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
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Q9mzp9
Q9mzp8
Q9mzp5
Q9mzp5
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09mzp2
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Q9mzq3
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STRAIN=BALB/C;
MEDLINB=20519697; PubMed=11063828;
MEDLINB=20519697; PubMed=11063828;
MOLIF M.E., Berman M.A., Tanabe S., Heesen M., Luo Y.;
"Astrocytes express functional chemokine receptors.";
J. Neuroimmunol. 111:109-121(2000).
EMBL; AF306532; AAK81712.1; -.
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Last annotation update)
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Q9rlv0 mus musculu
Q4244 oncorhynchu
Q9n0z0 cercocebus
Q9eq16 mus musculu
Q9bds6 macaca fasc
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2084.276 Million cell updates/sec
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Q9hca5 homo sapien
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Oglzh4 rattus norv
Og6a02 homo sapien
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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sp_human:*
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Maximum DB seq length: 2000000000
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Match Length DB
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colobus pol presbytis p presbytis f

presbytis e mandrillus

macaca assa

pygathrix a rhinopithec pygathrix n

mandrillus

pygathrix b nasalis lar

pongo pygma gorilla gor cercopithec cercopithec ö

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01-OCT-2001 (TrEMBLrel. 18, Last annotation update) CHEMOKINE RECEPTOR CCR9 (CC CHEMOKINE RECEPTOR 9A).
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                               Homo sapiens (Human)
                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                          Receptor.
SEQUENCE
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                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 IICFCVWMAAILLSIPQLVFYTVNDNARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLI 215
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        NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRIN-HARLAN SPRAGUE-DAWLEY;

Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;

"Identification and characterization of novel G-protein cougle and characterization of novel G-protein cougle (SEP-1998) to the EMBL, GenBank/DDBJ databases.

R EMBL; AFO90348; AAG24470.l.;

R InterPro; IPR000276; GPCR_Rhodpsn.

R PRINTS; PR00237; GPCRRHODDSN.

R PRINTS; PR00237; GPRRHODDSN.

R PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; UNKNOWN_1.
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                                                                                                     301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE G-PROTEIN COUPLED RECEPTOR GPCR14 (FRAGMENT).
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83.3%; Pred. No. 3.9e-73;
tive 19; Mismatches 15;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
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221 AA;
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01-MAR-2001
01-MAR-2001
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Yu C.-R., Peden K.W.C., Farber J.M.;
"CCR9A and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckbeta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGMQFLACISIDRYVAVTKVPSQSGVGKPCW-----IICFCVWMAAILLSIPQLVF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 YTVNDN---ARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 SSKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 IYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 IKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
MEDINE-99248139; PubMed-10229797;
MEDINE-99248139; PubMed-10229797;
Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
Ziaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
Ziaballication of the orphan chemokine receptor GPR-9-6 as CCR9,
receptor for the chemokine TECK.";
J. Immunol. 162:5671-5675(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 NQSTDYYYEE-NEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CC CHEMOKINE LARC SPECIFIC RECEPTOR.
MCCR6.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQIKEESGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKK
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.3%; Score 643; DB 4; Length 36 Best Local Similarity 36.4%; Pred. No. 4.5e-49; Matches 120; Conservative 75; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 AA; 42015 MW; F27CEA0CFB66B44C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AJ132337; CAB43477.1; ...
EMBL, AF145439; AAF66699.1; -.
INTETPRO: IPRO04069; Chemokine9_receptor.
InterPro: IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1531; CHEWOKINER9.
PRO1737; GPCRAHODOPSN.
PROSTITE; PSO0237; GPROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --YTVNDNARCIPIFPRYLGTS----MKALIQMLEICIGFVVPFLIMGVCYFITARTLMK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 MPNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCW----IICFCVWMAAILLSIPQLVF- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STDYYYEENEMNGTYDYSQYELI -----CIKEDVREFAKVFLPVFLTIVFVIGLAGNSM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CHEMOKINE RECEPTOR.
CHEMOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 KKYELQDRDVC---EPRYRSVSEPITWKLLGLGLELFFGFFTPLLFMVFCYLFIIKTLVQ
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Cloning of two chemokine receptor homologs (CXC-R4 and CC-R7) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99260342; PubMed-10331499;
Daniels G.D., Zou J., Charlemagne J., Partula S., Cunningham C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                            Specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 611; DB 11; Length 3
Pred. No. 3e-46;
0; Mismatches 124; Indels
                                                                                                                                                                                                                                             Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AB016031; BAA82443.1; -. HSSP; P34996; 1DDD. HSSP; P34996; 1DDD. InterPro; IPR000407; Chemokine6_receptor. InterPro; IPR000476; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1. PRINTS; PR01529; CHEMOKINER6. PRINTS; PR00237; GPCRRHODOPSN. PROSITE; PS00237; GPCRRHODOPSN. PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;
                                                                                                                                                                                         Molecular Cloning of Murine Homologue of CCR6, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 SIALFHSCLNPILYVFMGASFKNYVMKVAKKYGSWRRQRQ 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rainbow trout Oncorhynchus mykiss.",
J. Leukoc. Blol. 65:684-690(1999).
EMBJ. AJO03159; CAA05917.1; -
Interpro; IPR000276; GPCR.Rhodpsn.
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38.2%;
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042444;
01-JAN-1998 (TrEMBLEEL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 130; Conservative
                                                                                                                                                                                                                         for CC Chemokine LARC.
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                                                                                                                              SEQUENCE FROM N.A.
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042444
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Poehlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W., Kirchhoff {\bf F}_{\cdot, \cdot}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 LTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPIL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                 17 YDYDSSFTPTVGEDDVDNFMCDKSAVRAFRGQYEPPLYWSIVILGGLGNLTVVWIYLHPR 76
                                                                                                                                                                                                                                                                                                                                            22 YDYSQY------ELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecinae; Cercocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 LACISIDRYVAVTKVPSQSGVGKP----CWIICFCVWMAAILLSIPQLVFYTVND---NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kirchhoff F., "Son Doms R Kirchhoff F.," "Simian immunodeficiency virus utilizes human and sooty mangabey not rhesus macaque STRL33 for efficient entry.";
J. Virol. 74:5075-5082(2000).
                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                 Length 368;
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                                                                                                                                                                                                                                                                                     Indels
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Interpro; IPR000276; GFCR_Rhodpsn.
PRINTS; PR00237; GPCRHDODPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SEQUENCE 343 AA; 39589 MW; A75B7A0751C13455 CRC64;
                                                                                                                                             41523 MW; BE28E2D4C47E821A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                           Query Match 32.2%; Score 586.5; DB 13; Best Local Similarity 37.3%; Pred. No. 4.5e-44; Matches 120; Conservative 58; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 YVFVGVRFRRDILKLLRIYHCW 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 YVFMGASFKNYVMKVAKKYGSW 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                368 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matloubian M., David A., Engel S., Ryan J.E., Cyster J.G.;
"A transmembrane CXC chemokine is a ligand for HIV-coreceptor Bonzo.";
Wat. Immunol. 1:298-304(2000).
EMBL; AF301018; AAG34367.1; -.
MGD; MGI:1934582; Cxcr6.
InterPro: IPR000276; GPCR_Rhodpsn.
Prosite; PR00037; GPCRRHODOPSN.
PROSITE; PS00237; G_PCRRHODOPSN.
PROSITE; PS00237; G_PCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
                                                                          70 KKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQF 129
                                                                                                                    LACISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPQLVFYTV--NDNAR 183
                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 DGHYEGDFWLFNNSSDNSQ------BNKRFLKFKEVFLPCVYLVVFVFGLLGNSLVLII 64
                                                                                       DYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYY
                                                184 CIPIFPRYLGTSMKALIQMLEICIGEVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLL
                                                                                                                                                                        244 TVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILY
                                                                                                                                                                                                                    236 LVMAVFLLTQTPFNLVKLIRSTHWEYYAMTSFHYT-----ILVTEALAYLRACLNPVLY
                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                           304 VFMGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
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                   Indels
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Last annotation update)
                Mismatches 131;
        No. 2.4e-43;
                                                                                                                                                                                                                                                                                                                    351
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        Pred.
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MEDLINE-21177382; Pubmed-11017100;
33.78; Pt.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
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      Similarity
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Best Local Similarity
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SEQUENCE FROM N.A.

MEDLINE-21134756; PubMed-11242524;
Wade-Evans A.M., Russell J., Jahkins A., Javan C.;
Wade-Evans A.M., Russell J., Jahkins A., Javan C.;
"Cloning and sequencing of cynomolygus macaque ccr3, gpr15, and str133:
potential coreceptors for HIV type 1, HIV type 2, and SIV.";
AIDS Res. Hum. Retroviruses 17:371-375(2001).

EMBL, AR291671; AAK25742.1;
InterPro: IRR00276; GPCR_Rhodpsn.
Pfam; PP000017, 7tm.1.
PRINTS; PR00237; GPCRRHODPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNRNOWN_1.
                                               NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240
                                                                                    241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNP 300
SMLTLTCITVDRFIVVVQATKAFNRQAKWK-IWGQVICLLIWVVSLLVSLPQIIYGHVQD 183
                                                                                                                                                                                    301 ILYVEMGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSI 350
                                                                                                                                                                                                                                                                                      70 KKORTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQF 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 18, Last annotation update)
0R-OKT-2001 (TrEMBLRANE RECEPTOR STRL33.
MACACA fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LACISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPQLVFYTV--NDNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 AA; 39472 MW; 0961328F948E7784 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73; Mismatches 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          343 AA.
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Best Local Similarity 33.1%,
Matches 118; Conservative
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NCBI_TaxID=9541;
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SEQUENCE 343 AA; 394'
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MEDLINE-97311099; PubMed-9166430;
Liao F., Alkhatlb G., Peden K.W., Sharma G., Berger E.A., Farber J.M.;
"STRL33, A novel chemokine receptor-like protein, functions as a
fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-
                                                                                                                                                                                                                                    An P., Winkler C., O'Brien S.J.;
"The Influence of a STRL33 mutant on the course of HIV-1 infection.";
"The Influence of a STRL33 mutant on the course of HIV-1 infection.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF029759; AF021918 1.
Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PR00017; Tam_1 1.
PRINTS; PR000217; GPCRRHODDPSN.
PROSITE; PS000237; G_PROTEIN_RECEP_FI_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 LQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYINFYTSMLILT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPQLVFYTV--NDNARCI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 QRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLA 131
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STRAIN=STRL33(BONZO);
Brussel A., Pretet J.L., Girard M., Butor C.;
"Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and appri5 (BOB).";
AIDS Res. Hum. Retroviruses 15:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 YYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKK 71
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 VSLKFRKNFWKLVKDIGCLPYLGVSHQWKSSEDNSK--TFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 AA; 39279 MW; CE149633D01D20AA CRC64;
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Last annotation update)
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33.1%; Pred. No. 9.3e-42;
iive 75; Mismatches 130;
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EMBL; AF084229; AAD52041.1;
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                                                                                                                                                                        Exp. Med. 185:2015-2023(1997).
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NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sato H., Taniguchi M.;

"Molecular cloning of a putative chemokine receptor preferentially expressed in mouse lymphocytes.";

"Molecular cloning of a putative chemokine receptor preferentially expressed in mouse lymphocytes.";

submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF305709; AAG31284.1;

MGD; MGI:1934582; Cxcr6.

InterPro; IPR00027; GFCRRhodpsn.

PRINTS; PR00037; GFCRRHODPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.9%; Score 561.5; DB 11; Length 351; Best Local Similarity 35.4%; Pred. No. 7e-42; Matches 127; Conservative 69; Mismatches 126; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 AA; 40511 MW; B00E3134D2B4D1ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                             Last sequence update)
Last annotation update)
                                                               351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTANT G PROTEIN-COUPLED RECEPTOR STRL33
                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                               PRT;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-SPLEEN;
                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19, PUTATIVE CHEMOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                             PRELIMINARY;
                                                                                                                                                                                                                    musculus (Mouse).
                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
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Q9HCA5;
                                                             O9ERH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRL33
                  6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09HCA5
                    RESULT
                                         Q9ERH5
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Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
Q91ZH4
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                                                                                                                                                               8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A MEDLINE-2036847; Pubmed-10906389;
A Alabyev B.Y., Najakshin A.M., Mechetina L.V., Taranin A.V.;
Alabyev B.Y., Najakshin A.M., Mechetina L.V., Taranin A.V.;
Alabyev B.Y., Najakshin A.M., Mechetina L.V., Taranin A.V.;
T. "Claning of a CXCR4 homolog in chondrostean fish and characterization of a CXCR4 specific structural features.";
Dev. Comp. Immunol. 24:765-770(2000).
T. - SUNCELUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
C. -I. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR FMEL; AJ249438; CAB60252.1;
Interpro: IPRONO275; GPCR_Rhodpsn.
DR PROSITE; PSO0237; GPCRRHODOPSN.
DR PROSITE; PSO0237; GPCRRHODOPSN.
DR PROSITE; PSO0237; GPCRTEIN RECEP_FL.1; 1.
DR PROSITE; PSO0237; GPROTEIN RECEP_FL.2; 1.
KW G-PFOCHAIN COUPLED RECEP_FL.2; Transmembrane.
SO SEQUENCE 358 AA; 40448 MW; 7B3B99B962453008 CRC64;
                                                                                                                                                                                                                                                                                                   132 CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPQLVFYTV--NDNARCI 185
                                                                                                                                                                                                                                                                                                                        72 QRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLA 131
                                                                                                                                                                                                                                                               6 YHEDYGFNSFNDSSQEE----HQDFLQFSKVFLPCMYLVVFVCGLVGNSLVLVISIFYHK 61
                                                                                                                                                                Gaps
                                                                                                                                                                                     12 YYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                         186 PIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTV
                                                                                                                                                                                                                                                                                                                                                                                181 ----GYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLV
                                                                                                                                                                                                                                                                                                                                                                                                                     246 VIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Chondrostei, Acipenseriformes, Acipenseridae,
Acipenserinae, Acipenser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 VSLKFRKNFWKLVKDIGCLPYLGVSHQWKSSEDNSK--TFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 MGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                                                                                                                             32;
                                                                                                                                  Length 342;
                                                                                                                                                          74; Mismatches 131; Indels
                                                                                     5B58003797806B2A CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
             Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                               30.7%; Score 559; DB 6; 33.1%; Pred. No. 1.1e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
InterPro; IPR000276; GPCR_Rhodpsn
                                                                                       342 AA; 39273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acipenser ruthenus (sterlet).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                               Query Match 30.7%
Best Local Similarity 33.1%
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHEMOKINE RECEPTOR 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                        Receptor.
SEQUENCE
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Q9PUA0
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Length 358;

Score 544; DB 13; Pred. No. 2.6e-40;

29.9%;

Query Match Best Local Similarity

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9
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                                                                                                                                                                        67 AYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSG 126
                                                                                                                                                                                                                                            127 MQFLACISIDRYVAVTKVPSQSGVGKPC----WIICFCVWMAAILLSIPQLVFYTVNDN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                           7 TVDFTFENNTEGSGSGDTSQYDEVCKRNLNGDLRKIFLPTVYTIIFVMGIVGNGLVVIVM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-C CHEMOKINE RECEPTOR 4...
Ratius norvegicus (Rat).
Eukaryota; Metazoa; Chondata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=LEW;
Garcia G.E., Chen S., Xia Y., Harrison J., Wilson C.B., Johnson R.J.,
Bacon K.B., Feng L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 VAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVSGMQFLACISIDRYVAVTKV-----PSQSGVGKPCWIICFCVWMAAILLSIPQLVF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 YTV---NDNARCIPIFPRYLGTSMKALIQMLEI-CIGFVVPFLIMGVCYFITARTLMKMP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 STDYYYEEN-EMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                              238 PLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 ALKTIILILAFFICWLPYCIAILVDTLVLLNVIQYNCTLQHHMETWIFVTEGLAYFHCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 A---RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMK-MPNIKISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYSGIFFIMLMSIDRYLAIVHAVFSLRARTLTYGV----ITSLITWSVAVFASLPGLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.4%; Score 534.5; DB 11; Length 360; 34.7%; Pred. No. 1.8e-39; ive 67; Mismatches 127; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 LNPILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFS 349
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF432872; AAL30398.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AA; 41218 MW; 5095C6CD299E1F8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
64; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
Conservative
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Best Local Similarity 34.77
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Search completed: August
Job time: 143 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 MVLLRYVPRRRWVEIYLLNLAISNLLFLVTLPFWGISVAWHWVFGSFLCKMVSTLYTINF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 YSGIFFISCMSLDKYLEIVHAQPYHRLRTRAKS-----LLLATIVWAVSLAVSIPDM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 MPNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 LRPAGGGRALKIAAALVVAFFVLWFPYNLTLFLHTL-LDLQVFGNCEVSQHLDYALQVTE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 AIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 VSGMQFLACISIDRYVAV-----TKVPSQSGVGKPCWIICFCVWMAAILLSIPQL 173
NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 SENSSFYY-----YDYLDEVAFMLCRKDAVVSFGKVFLPVFYSLIFVLGLSGNLLLL 68
              OJEGNO.

01-DEC-2001 (TrEMBLrel. 19, Created)

01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

01-DEC-2001 (TREMBLrel. 19, Last annotation update)

UNIXIOWN (PROTEIN FOR MGC:10475) (PROTEIN FOR MGC:10537).

Homo sapiens (Human).

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;

Mammalla: Eutherla: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOSTDYYYEENEMNGTYDYSQYE--LICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 VFYTVNDNAR-----CIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.0%; Score 527; DB 4; Length 384
32.9%; Pred. No. 8.8e-39;
:ive 72; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                    Straubberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011631; AAH11631.1; -.
EMBL; BC008816; AAH08816.1; -.
SFOURNCE 384 AA; 43442 MW; 464C5703C1DE9A6A CRC64;
                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                           384 AA.
                                                                                                                                                                                                                                                                                               TISSUE-PLACENTA, AND CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                            TISSUE-PLACENTA, AND CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                 | | | | | | | | : | | : | | : | : : | AFIHCCLNPVIYFELGEKFRKYIAQL 318
                                                 292 ALFHSCLNPILYVFMGASFKNYVMKV 317
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 SIALFHSCLNPILYVFMGASFKNYV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9YGC3 PRELIMINARY;
O9YGC3;
O1-MAY-1999 (TrEMBLrel. 10, Cz
O1-MAY-1999 (TrEMBLrel. 10, La
O1-JUN-2001 (TrEMBLrel. 17, La
CHEMOKINE RECEPTOR 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 29.0
Best Local Similarity 32.9
Matches 107; Conservative
                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    NCBI_TaxID=9606
                                                                                                                                       096A02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
Q9YGC3
232
                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299
                                                                          293
                                                                                                                RESULT
Q96A02
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79 YILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLACISIDRY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 LAIVHAINSQGSRKMLADKVVYAGVWLPALLLIVPDLVFARVSDENGQFVCDRIYPIENR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAVTKVPSQSGVGKPC--WIICFCVWMAAILLSIPQLVFYTVND-NAR--CIPIFPRYLG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 NGSGDFEDFIEPCFMHENSDFNRIFLPTIYSFIFLLGIIGNGLVVVWGYQKKSRTWTDK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 NGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKKQRTKTDV 78
                                                                                                                       ETWTVGFRFLHITVGLILPGLIILICXCVIISKLSHSKGHQKRKALKTTVILILAFFACW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPYNIVKFCRAID--IIYSLIT-SCNMSKRMDIAIQVTESIALFHSCLNPILYVFMGASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 TSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTVVIVFIVTQ
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.6%; Score 520.5; DB 13; Length 358; 35.9%; Pred. No. 3.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Mismatches 121;
laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                  Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 108; Conserv
                                                                                                       SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 K 311
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6, 2002, 18:09:28

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	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - pro	OM protein - protein search, using sw model
Run on:	August 6, 2002, 18:05:40 ; Search time 17.74 Seconds (without alignments) 1895.787 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-686-020A-2 1819 1 MALEQNQSTDXXXEENEMNGVEEFPFDSEGPTEPTSTFSI 350
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	283138 seqs, 96089334 residues

283138

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000

Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

G protein-coupled lymphocyte specifi g protein-coupled g protein-coupled chemokine (C-C) re interleukin-8 rece probable G protein-coupled g protein-coupled g protein-coupled interleukin-8 rece interleukin-8 rece neuropeptide Y/pep fusin (LESTRA) - C chemokine (C-C) re interleukin-8 rece interleukin-8 rece G protein-coupled macrophage inflamm chemokine (C-C) re interleukin-8 rece interleukin-8 recept in chemokine (C-C) re interleukin-8 rece G protein-coupled chemokine (C-C) re interferon-inducib Description SUMMARIES JN0621 BB55735 A45680 JC5068 A57160 A57161 JC4597 JC4597 A5747 S28787 S28787 S28787 S28787 S28787 S2845 JC2443 JC2443 JC2443 A5747 S28787 JC5067 JC50 A43113 A48921 138450 149341 JE0349 A45177 S42096 S55594 G02436 DB % Query Match Length D 2299. 2299. 2299. 2299. 2299. 2299. 2399. 2499. 2599. 484.5 483.5 482 479.5 476.5 Score Result ₽.

anglotensin II rec	angiotensin II rec	angiotensin II rec	angiotensin II rec	G protein-coupled	anglotensin II rec	MIP-1 alpha recept	G protein-coupled	G protein-coupled	angiotensin II rec	angiotensin II rec	angiotensin II rec	G protein-coupled	MDCR15 protein - h	angiotensin II rec	angiotensin II rec
S44425	JC1104	JC2134	S15403	S32785	A48857	149340	S26667	S42628	JN0694	A42656	JH0621	A39714	S56162	JQ1516	139418
7	~	~	N	~	~	N	~	~	~	~	~	7	~	~	7
359	359	359	359	374	359	356	372	374	362	359	359	362	327	359	359
25.0	24.9	24.9	24.7	24.7	24.5	24.5	24.3	24.3	24.2	24.1	24.1	24.1	24.1	23.9	23.6
455.5	452.5	452.5	450	450	446.5	445.5	442.5	442.5	441	439	438.5	438.5	437.5	434	428.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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G protein-coupled receptor EBII - mouse
C;Species: Mus musculus (house mouse)
C;Caccession: A55735
C;Accession: A55735
C;Acces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
A45680
G protein-coupled peptide receptor EBI'1 - human
C; Species: Homo sapiens (man)
C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C; Accession: A45680
R; Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A/Title: Epstein-Barr Virus-induced genes: first lymphocyte-specific G protein-couple
A; Reference number: A45680; MUID: 93188173
A/Title: Epstein-Barr Virus-induced genes: first lymphocyte-specific G protein-couple
A; Reference number: A45680; MUID: 93188173
A/Accession: A45680
A; Accession: A45680
A; Accession: B4580
A; Accession: B4580
A; Residues: 1-378 calra
A; Residues: B-1378 calra
A; Residues: B-1378 calra
A; Residues: B-1378 calra
A; Residues: B-1378 calra
A; Experimental source: B-1ymphocytes
A; Note: sequence extracted from NOBI backbone (NCBIN:127094, NCBIP:127095)
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGMQFLACISIDRYVAVTKVPSQSG------VGKPCWIICFCVWMAAILLSIPQLVFYT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IALFHSCLNPILYVFMGASFKNYVMKVAKKYGSWRRQR------QSVEEFPFDSEGPTE 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.7%; Score 650; DB 2; I larity 38.3%; Pred. No. 2.7e-48; Conservative 67; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 643; DB 2;
No. 1.1e-47;
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Pred.
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Best Local Similarity
Matches 140; Conserv
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A: A: Testauces: 1-3.0 s.c.n.
A: A: Testauces: GB: Li31581; NID: 9468319; PIDN: AAA74231.1; PID: 9468320
B: Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
B: Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
B: Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
B: Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
A: Accession: S52443
A: Molecule type: DNA
A: Residues: 21-378
A: Molecule type: DNA
A: Residues: 21-378
A: Gene: GDB: CMRBR7; EBIL; BLR2; CCR7
A: Gene: GDB: CMRBR7; EBIL; BLR2; CCR7
A: Map position: 17q12-17q21.2
C: Superfamily: vertebrate rhodopsin
C: Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B55735; S52443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Arītle: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor A;Reference number: A55735; MUID:95154835
                                                                                                                                                                                                                                                                  lymphocyte-specific G protein-coupled receptor EB11 - human
N.Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                        Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 2;
4.5e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 659;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.2%; Scor
38.7%; Pred
tive 66; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 36.2%
Best Local Similarity 38.7%
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 SEGPTEPTSTFS 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
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A; Gene: CDB: CMKBR4
A; CTOSS -references: GDB: 677463
A; Map position: 3p21-3p21
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM2>
E; 10-65/Domain: transmembrane #status predicted <TM3>
F; 112-13f/Domain: transmembrane #status predicted <TM3>
F; 112-13f/Domain: transmembrane #status predicted <TM4>
F; 201-26f/Domain: transmembrane #status predicted <TM5>
F; 201-26f/Domain: transmembrane #status predicted <TM6>
F; 201/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I. J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor A;Reference number: A57160; MUID:95370289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERIAL STANFARM STANKALSSLEINILGEVIPLGIMLFCYSMITRTLQHCKNEKKNKA 240
   MQFLACISIDRYVAVTKVPS----QSGVGKPCWIICFCVWMAAILLSIPQLVF---YTVN 179
                                                                                                                                                                                                                                                                                                          245 HKAIRVIIAVVLVFLACQIPHNMVLLVTAAN-LGKMNRSCQSEKLIGYTKTVTEVLAFLH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 VMLMSIDRYLAIVHAVFSLRARTLTYGV----ITSLATWSVAVFASLPGFLFSTCYTER 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A;Note: source clone K5-5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                           GSDVC---EPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFMIFCYTFIVKTLVQAQNSKR
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                                            MLLTCISMDRYIAIVQATKSFRLRSRTIPRSKIICLVVWGLSVIISSSTFVFNQKYNTQ
                                                                                                                     DNARCIPIFPRYLGTS----MKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKI
                                                                                                                                                                                                                                              236 SRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFH
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                                                                                                                                                                                                                                                                                                                                                                                                   304 CCLNPVLYAFIGQKFRNYFLKILKDLWCVRRKYKS 338
                                                                                                                                                                                                                                                                                                                                                                       SCLNPILYVFMGASFKNYVMKVAKKYGSWRRQRQS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemokine (C-C) receptor 4 -
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C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like
A;Reference number: JC5067; MUID:97040707
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   8;
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A; Residues: 1-369 - 2AB->
A; Cross-references: EMBL:279784; NID:g1668737; PIDN:CAB02144.1; PID:g1668738
C; Comment: This protein belongs to the family of alpha chemokine receptors.
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                                                                                                                                                                                  MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
                                                                                                                                                                                                                                                                                                       LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWII--CFCVWMA--AILLSIPQLVFY 176
                                                                                                                                                                                                                                                                                                                                                                                                                          177 TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP 231
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                         CLCQDEVIDDYIGDNT---TVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYA 67
                                                                                                                                                                                                                                                                                                                                          ALFHSCLNPILIYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD
                                                               MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 ACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVE----
   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
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A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
C; Superfamily: Vertebrate rhodopsin
C; Superfamily: Vertebrate #status predicted <TM3>
F; 19-99/Domain: transmembrane #status predicted <TM4>
F; 115-133/Domain: transmembrane #status predicted <TM4>
F; 112-233/Domain: transmembrane #status predicted <TM6>
F; 212-233/Domain: transmembrane #status predicted <TM6>
F; 220-211/Domain: transmembrane #status predicted <TM6>
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36.1%; Pred. No. 1.5e-42;
ive 68; Mismatches 120; Indels
   Mismatches 127; Indels
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predicted <TM7>
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62;
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Best Local Similarity 36.19
Matches 121; Conservative
   Conservative
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   145;
   Matches
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C.Species: Rattus norvegicus (Norway rat)
R.Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A.Fitle: CDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord an A.Faccession: IS8186; MUID:94323113
A.Faccession: IS8186
A.Species: Rattus preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-354 <RES>
A.Residues: 1-354 <RES>
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                orphan G protein-coupled receptor - human
N:Alternate names: V28 protein
C;Species: Homo sapiens (man)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C;Accession: JQ4304
                                                            MKMPNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQV 287
                                                                                                                                                                                                                                                                                                               F----YTVNDNARCIPIFPRYLG---TSMKALIQMLEICIGFVVPFLIMGVCYFITARTL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 NLAVADLLLEFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLACISIDRYVAV 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314
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                                                                                                                                                                                         288 TESIALFHSCLNPILYVFMGASFKNYVMKVAKKYGSWRRQ---RQSVEEFPFDSEGPTEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable G protein-coupled receptor - rat
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Best Local Similarity
Matches 113; Conserv
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C; Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C; Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C; Accession: 137898; I38712; A53611; A39446
R; Ahula, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. B101. Chem. 269, 26381-26389, 1994
A; Title: Comparison of the genomic organization and promoter function for human interlet A; Reference number: 137898; MUID:95014476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Accession: A53611
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residuas: 6-360 < Spray
A; Cross-references: 6B:M99412; GB:L19593
B; Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A; Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Across references: EMBL:U11872; NID:9511808; PIDN:AAA64380.1; PID:9511809; EMBL:U11873; I1876; NID:9511816; PID:9511817; EMBL:U11877; NID:9511818; PID:9511819; EMBL:U11878; NID:87 PID:9511819; EMBL:U11878; NID:87 PID:9511819; EMBL:U11878; NID:87 PID:9511819; EMBL:U11878; NID:97 PID:97 PI
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A;Residues: 6-360 <MUR>
A;Cross-references: GB:M73969
C;Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8,
C;Genetics:
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8
LKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCL 298
                                        A; Molecule type: DNA
A; Residues: 1.360 <RES>
A; Cross-references: EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g511803
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A;Map position: 2435-2435
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A39446; MUID: 91368200
A; Accession: A39446
                                                                                                                                                                                                                                                                                                                                                    interleukin-8 receptor type B - human
                                                                                                                         299 NPILYVFMGASFKNYVMKVAK 319
                                                                                                                                                                        Query Match
Best Local Similarity 33.2%
Matches 120; Conservative
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A Status: preliminary
A Molecule type: mRNA
A:Residues: 1-15 <RE2>
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Length 360;

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F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted F;72,202,300/Bainding site: phosphate (Ser) (covalent) (by casein kinase II) #status p:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Correction coupled receptor GPR2 - human (fragment)
Correction: Homo sapiens (man)
Correction: Homo sapiens (man)
Correction: 1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999
Correction: 185973
Correction: 1859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 VAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVSGMQFLACISIDRYVAVTKV-----PSQSGVGKPCWIICFCVWMAAILLSIPQLVF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 KORTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMOFL 130
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                                                                                                                                                                                                                                                                                                                                                                         176 STCYTEHNHTYCKTQYS--VNSTTWKVLSSLEINVLGLLIPLGIMLFWYSMIIRTLQHCK
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                                                                                                                                                                                                                                                                                                                                    3 LEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI
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                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                               69; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                  Score 522.5; DB : Pred. No. 2.3e-37
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Pred. No. 5e-37;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 GFIHCCLNPVIYFFLGEKFRKYITQL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 ALFHSCLNPILYVFMGASFKNYVMKV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GDB:371708; OMIM:66
A; Map position: 17421.1.17421.3
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65;
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C;Genetics:
                                                                                                                                                                                                                                    Similarity
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Best Local Simi
Matches 121;
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                                                                                                                                                                                                     Query Match
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                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-355 < RAPP
A; Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A; Experimental source: peripheral blood mononuclear cell
C; Comment: This protein is a cell-surface receptor which recognizes extracellular signal
C; Comment: This protein is a key regulator of many immune and homeostatic responses, and
C; Genetics:
A; Gene: v28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ដ
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C; Species: Mus musculus (house mouse)
C; Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C; Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C; Accession: JG4587
R; Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A; Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines A; Reference number: JG4587; MUID:96136324
                                                                       related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLACISIDRYVAV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 NLALSDLLFVATLPFWTHYLINEKGLHNAMCKFTTAFFFIGFFGSIFFITVISIDRYLAI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 TKVPS-----QSGVGKPCWIICFCVWMAAILLSIPQLVFYTVNDNARCIPIFPRYLGT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254
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Gene 163, 295-299, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 SMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTVVIVFIVTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILYVFMGASFKNYV
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C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
                                                                                                                                                                                                                                                                                                                                                                                                                      A super position: 3pter-p21
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superds: G protein-coupled receptor; lymphokine; tran
E; 35-57/Domain: transmembrane #status predicted <TM1>
E; 66-88/Domain: transmembrane #status predicted <TM2>
E; 104-125/Domain: transmembrane #status predicted <TM3>
E; 145-217/Domain: transmembrane #status predicted <TM3>
E; 197-217/Domain: transmembrane #status predicted <TM5>
E; 230-254/Domain: transmembrane #status predicted <TM5>
E; 275-296/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.7%; Score 522.5; DB 2; Best Local Similarity 36.4%; Pred. No. 2.3e-37; Matches 112; Conservative 57; Mismatches 122;
                                                                                                                              A; Accession: JC4304
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29;

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Length 355;

27.6%; Score 501.5; DB 2; 33.1%; Pred. No. 1.4e-35; tive 70; Mismatches 127;

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A; Molecule type: DNA
A; Residues: 1-355 <BEC>
A; Cossidues: 1-364, 1992
A; Title: Characterization of complementary DNA clones encoding the rabbit IL-8 recept A; Accession: A46483; MUID: 92148149
A; Accession: A46483
A; Status: preliminary
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 YAYYKKQRTKTDVYILNLAVADLLLETLPFWAVNAVHGWVLGKIMCKITSALYTLNFVS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 YYEENEMNGT-----YDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441 A;Experimental source: neutrophils
A;Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530) C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 107; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inferleukin-8 receptor (clone 5Bla) - rabbit (Species: Orycologus cuniculus (domestic rabbit) (Species: Orycologus cuniculus (domestic rabbit) (Species: Orycologus cuniculus (domestic rabbit) (Species: Orycologus cuniculus) (domestic rabbit) (Species: Orycologus) 
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus
C;Species: Oryctolagus
R;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyma
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A;Title: Molecular characterization of the interleukin-8 receptor.
A;Reference number: J01231; MUID:91378994
                 CIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLL 243
                                                                            244 TVVIVEIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILY 303
                                                                                                                                                                                                                                        GNSMVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 LVFYTVNDNARCIPIFPRYLGTS---MKALIQMLEICIGFVVPFLIMGYCYFITARTIMK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 MPNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTE 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-358 <PRA>
A; Cross-references: GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                       8 NYSYE--DFFG--DFSNYSYSTDLPPTLLDSAPCRSESLETNSYVVLITYI-LVFLLSLL
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Best Local Similarity
Matches 116; Conserva
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N.Alternate names: fusin; HM89; leukocyte-derlved seven-transmembrane receptor LESTR; C.Speciaes: Homo sapiens (man)
C.Speciaes: Homo sapiens
C.Speciaes: Homo s
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A/Molecule type: mRNA
A/ECOSTION: A53103
A/Molecule type: mRNA
A/ECOSTION: A532 CLOS: A532
GMQFLACISIDRYVAV --- TKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVNDNA 182
                                                                                                              RCIPIFPRYLG----TSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPL
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Search completed: August
Job time: 192 sec
  A; Residues: 1-353 <RIM>
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FLGAKFK 311
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                                            A; Status: preliminary; translated from GB/EWBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: 1-352 cHER>
A; Molecule type: 1-352 cHER>
A; Molecule type: 1-352 cHER>
A; Cross-references: GB:L06797; NID:9414929; PIDN:AAA03209.1; PID:9414928
R; Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.; Lar
A; Jitle: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homolc
A; Reference number: 159444; MUID:94052833
                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mSNA
A;Cross-references: GB:L01639; NID:g189313; PIDN:AAA16594.1; PID:g189314
B;Nomura, H.; Nielsen, B.W.; Matsushima, K.
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem A;Reference number: 154751; MUID:94092629
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
C;Accession: S28787
C;Accession: S28787
Mol. Pharmacol. 40, 869-875, 1991
A;Title: Sequence and expression of a neuropeptide Y receptor CDNA.
A;Reference number: $28787; MUID: 92100053
A;Accession: S28787
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :| | : | | : | 185 ICDRFYPNDLWV---VVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTT 241
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A;Map position: 2q21-2q21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: 169203
A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA
A; Residues: 1-352 < RES>
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A; Reference number: I53006; MUID: 93319629
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YAFLGAKFK 310
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RTKTDVYILNLAVADLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLAC 132
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                                                                                                                                                                                                                                                                                                                                                                           133 ISIDRYVAVTKVPSQSGVGKPC----WIICFCVWMAAILLSIPQLVF---YTVNDNARC 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A.Cross-references: EMBL:M86739
C;Superfamily: vertebrate rhodopsin
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein
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                                                                                                                Length 353;
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                                                                                                            27.5%; Score 499.5; DB 2; 34.5%; Pred. No. 2.1e-35; iive 60; Mismatches 126;
                                                                                                       Query Match 27.5%
Best Local Similarity 34.5%
Matches 106; Conservative
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